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| Li,Y.<br>containing molecula | itae; Streptophyta;<br>liophyta; eudicotyl<br>; I; Solanales; Sol              | 157             | 456 bp                             | ALIGNMENTS | AC006269 | ACU22281<br>AL365354 | AF151388  | PFMAL4P4<br>DDI301668  | CNS07ECV  | HS1100E15  | CNS01RGG | AL590287   | AL136178 | AC079621  | AC080091<br>HSKB152G3 | AC117073  | AL359832   | AC104069  | AC011463  | AC105252             | PFMAL4P2  | AL627305<br>AF141654 | AX346470 | AX281353 | AC087568 | AL593856  | NSCHRIB  | NTT85A<br>AR059252 | TOBPSAEB | AR059248           | AR059249 | AR059251 | AX467562 | ID          | SOMETIMES | STIMMARTES |
| ular decoys                  | ohyta; Em<br>cotyledo  |                 | DNA                                |            |          |                      |           |                        |           |            |          |            |          |           |                       |           |            |           |           |                      |           |                      |          |          |          |           |          |                    |          |                    |          |          |          |             |           |            |
| that alte                    | .a; Embryophyta; Tr<br>.yledons; core eudi<br>.olanaceae; Nicotia              |                 | linear PAT                         |            | AC006269 | AC022281<br>AL365354 | AF151388  | AL035477<br>AJ301668   | AL442663  | AL035551   | AL157971 | AL590287   | AC006132 | AC079621  | AC080091<br>AL132982  | AC117073  | AL359832   | AC104069  | AC011463  | AC105052<br>AC105252 | AL035475  | AL627305<br>AF141654 | AX346470 | AX281353 | AC087568 | AL593856  | X57079 N | X70902 N           | D42070 T | AR059248           | AR059249 | AR059251 | AX467562 | Descript    |           | •          |
| r protein                    | phyta; Tracheophyta;<br>core eudicots;<br>;; Nicotiana.                        |                 | 16-JUL-2002                        |            | Homo     | Homo sapi            | Dermatobi | Plasmodiu<br>Dictvoste | Human chr | Human DNA  |          | Human DNA  | Huma     | Homo sapi | Homo sapi             | Dictyoste | U I        | Homo sapi | Homo sapi | Homo sapi            | Plasmodiu | Nicotiana            | Sequence | Seque    | Pan tro  | Human DNA | sylves   | Sequence           | bacco ps | 9 2                | Sequence |          | Sequenc  | ģ           |           |            |

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: Perfect score: Sequence: Database : Post-processing: .Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seg length: 0
Maximum DB seg length: 2000000000 Total number of hits satisfying chosen parameters: Searched: Scoring table: OM nucleic - nucleic search, using sw model Run on: US-09-941-042C-1 456 June 9, 2003, 07:09:40; Search time 1534 Seconds
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8651.160 Million cell updates/sec IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0 2054640 seqs, 14551402878 residues GenEmbl: \* ggaaacatattcaatacatt.....ggtaaaaagcagttacagag 456 gb\_ba:\* em\_htgo\_hum:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| REFERENCE<br>AUTHORS<br>TITLE  | SOURCE<br>ORGANISM  | ACCESSION<br>VERSION | RESULT 1 AX467562 LOCUS |            | C 44 6               |          | 41                   |           | . ω<br>ο œ |          |           | 10<br>14<br>14<br>16 | k         |                    | ພ ຍ<br>ວ 9            |          | 26                  | 25       |          |                      |                    |  |                    | 15                | 14 6                 |                   | 110        | •        | 18                    |          |                                     |          |  | Result<br>No. Sc |
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| 1<br>Conkling,M.<br>Transgenic | . common tobac Nicotiana ta Eukaryota; \ Spermatophyt Asteridae; 6              |                      | ,                       |            | 13.6                 |          |                      |           |            |          |           |                      |           |                    |                       |          |                     |          |          |                      |                    |  |                    |                   |                      |                   |            |          |                       |          |                                     |          | 88                                     | Query            |
| M.A. and<br>c plants           | Day<br>Thr  | GI:2                 | 5                       |            | 106090<br>167362     | 198853   | 1792                 | 1266      | 165423     | 165260   | 103344    | 110000               | TRCKOT    | 145598             | 91798<br>96953        | 158813   | 155711              | 195130   | 44067    | 101944               | 152797             | 3945                                     | 149497             | 5145              | 5145                 | 116696            | 157373     | 722      | 2347<br>6053          | 2010     | 1988                                | 1294     | 456<br>1030                            | Length           |
|                                | Ldiplanta<br>Magnolio<br>sterids I.   | 190075               | †<br>†                  |            | NU                   |          |                      |           |            |          |           |                      |           |                    |                       |          |                     |          |          |                      |                    |  |                    |                   |                      |                   |            |          |                       |          |                                     |          |  | 8                |
| Y.<br>taining molecular        | a; Streptophyta<br>phyta; eudicot;<br>; Solanales; So                           | 7                    | 456 bp DNA              | ALIGNMENTS | AL732577<br>AC006269 | AL365354 | AF151388<br>AC022281 | DDI301668 | CNS07ECV   | AC024341 | HS1100E15 | PEMAL4P1_1           | AI.590287 | AC008132           | HSKB152G3<br>AC079621 | AC080091 | VYIVD10<br>AC117073 | AL359832 | AL357136 | AC103232<br>AC011463 | AC108052           | AF141654<br>PFMAL4P2                     | AL627305           | AX345250          | ACU6/366<br>AX281353 | PFWAL3P3          | AL593856   | AR059252 | NTT85A                | AR059247 | AR059249<br>AR059248                | AR059250 | AX467562<br>AR059251                   | ID               |
| decoys that alter protein      | ; Embryophyta; Tracheophyta;<br>ledons; core eudicots;<br>blanaceae; Nicotiana. |                      | linear PAT 16-JUL-2002  |            | domo                 | omo      | ğĕ                   | Mety      | řĒ         | ğ        | uman      | on                   | lumai     | ACOO8132 Homo sapi | domo d                | ğ        | Lagr                | Ē        |          | ACC011463 Homo sapi  | AC108052 Homo sapi | AF141654 Nicotiana<br>AL035475 Plasmodiu | AL627305 Danio rer | AX345250 Sequence | eq                   | 298547 Plasmodium | uma<br>Y L | eque     | X70902 N. tobacco psa | sequence | ARUS9249 Sequence ARUS9248 Sequence | equen    | AX467562 Sequence<br>AR059251 Sequence | Description      |

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Conkling, M.A., Mendu, N. and Song, W. Root cortex specific gene promoter Patent: US 5837876-A 3 17-NOV-1998;
Location/Qualifiers
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Conkling,M.A., Mendu,N. and Song,W. Root cortex specific gene promoter Patent: US 5837876-A 1 17-NOV-1998;
Location/Qualifiers
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                                            Unclassified
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Conkling,M.A., Mendu,N. and Song,W.
Root cortex specific gene promoter
Patent: US 5837876-A 2 17-NOV-1998;
Location/Qualifiers
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Nicotiana sylvestris (library: lambda DASH) DNA, clone KuEG3
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                                                                                                                                                                                                                                                                                   D42070
D42070.1 GI:575606
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                                        Obokata, J.
Direct Submission
Submitted (09-NOV-1994) Junichi Obokata, Hokkaido University,
Submitted (09-NOV-1994) Junichi Obokata, Hokkaido University,
Sapporo, Hokkaido
Graduate School of Environm. Earth Sci.; kita-ku, Sapporo, Hokkaido
060, Japan (E-mail:jo@cul.hines.hokudai.ac.jp, Tel:011-706-5291,
Fax:011-757-5994)
                                                                                                                                                              Nicotiana sylvestris
Plant Physiol. 108 (
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                                             Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 6053)
                                                                                                 auxin binding protein; Nicotiana tabacum.
                                                                                                                                  N.tobacum
x70902
 Direct Submission Submitted (19-JAN-1993) S. Agrobiological, Resources,
                                                                                                                         X70902.1
                                                                                                                                                        NTT85A
                                  Shimomura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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nilarity 83.5%;
Conservative
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/number=2
2018. .2274
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/gene="psaEb"
Join(1125. .1397,1853. .1918,2018.
/gene="psaEb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="KuEG3"
/clone_lib="lambda DASH"
1090. .1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGVGSVVAVDQDPNTRYPVVVRFNKVNYANVSTNNYALDEVEEVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="masssmasaasgemvatpniatsntaprtsmlfesssknntttn
fprlvvraaeeaappaatataegeappakaakpppigpkrgtkvstpvrvlrkesymv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="PSI-E subunit of
/protein_id="BAA07667.1"
/db_xref="GI:1217601"
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                                                                                                                                               T85
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Pred. No. 5.9e-28;
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                                                                                                               T85
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Kannondai
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    , National Institute
2-1-2, Tsukuba, Ibar
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2 (bases 1 to 6053)
Watanabe, S. and Shimomura, S.
Cloning and expression of two genes encoding auxin-binding proteins
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                                             Similarity
                                 40.4%;
nilarity 74.2%;
Conservative (
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/number=1
/evia-
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4947. .>5448
/gene="T85"
                                                                                                                                                                                                                                                                                3213. .3416
/gene="T85"
                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MARHYLVVVAVLLEATAEASQCSINGLPLVRNISELPQENYGRS
GLSHTTIAGSVLHGMKEIEVWLQTFAPGSRTPIHRHSCEEIFVVLKGQGILYLTPSSH
SKYPGNPQEFHIFPNSTFHIPVNDVHQVWNTGEHEDLQVLVVISRPPVKVFMYDDWSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=experimental
join(2193. .2268,2641.
4947. .5055)
                                                                                                                                                         4200. .4946
/gene="T85"
                                                                                                                                                                                                    4132. .4199
/gene="T85"
                                                                                                                                                                                                                                                                                                                 /evidence-experimental
2748. .3212
/gene-"T85"
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/protein_id="CAA50259.1"
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/clone="lambda T85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Nicotiana tabacum"
/cultivar="NK326"
                                                                                        /evidence-experimental
1027 c 1034 g 2041
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                                  Score 184.2; DB 8;
Pred. No. 5.5e-19;
0; Mismatches 98;
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                                                        Length 6053;
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Sequence 6 :
AR059252
 NSCHRIB 5040 bp DNJ
N.sylvestris DNA for 31kD chloroplast
X57079 S38099 S38103 S38111 S38122
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108 c 129 g
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1047 AAACATATTTATTTGCTACTCATAATCGCTACAATACCTTGTGTCTTAGCTTGCTAGTTA 1106
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Conkling,M.A., Mendu,N. and Song,W.
Root cortex specific gene promoter
Patent: US 5837876-A 6 17-NOV-1998;
Location/Qualifiers
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                                                                                CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACTCCTAGTTG
                                                                                                                                                                                                                                                                     32.5%; Score 148; DB 6; 100.0%; Pred. No. 2.6e-13;
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US 5837876.
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              linear
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           PLN 29-NOV-1993
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Nicotiana sylvestris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 5040)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-DEC-1990) M. Sugiura, CEN NAGOYA UNIVERSITY, NAGOYA 464-01, JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCCTAGAATACTTTGTGCCTT
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                                                  Conservative
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EEEGFVEAVGDAGESDEVEADEEEEEEFQEPPEDAKLFVGNLPYDVDSEGLARLFEQAG
VVEIAEVIYNRDTDQSRGFGFVTMSTVEEAEKAVEMYNRYDVNGRLLTVNKAARRGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="31kD chloroplast ribonucleoprotein"
/protein_id="CAA40364.1"
/db_xref="GI:19741"
                                                                                                                             /evidence=experimental
777 c 897 g 1
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join(2099. .2596,2830.
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/db_xref="taxon:4096"
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3728. .4577
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?830. .2931
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                                                                 20.7%;
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                                                                 Score 94.4; DB 8; Pred. No. 1.5e-05;
                                                  Mismatches 116;
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                                                                                Length 5040;
                                                  Indels 16;
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                    60
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AUTHORS
TITLE
JOURNAL
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SOURCE
ORGANISM
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AL593856/c
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FEATURES
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1222 GTAAAGATATTTAATACCTTATGGTTTGATACTCAAGATCGCCAAATTAC-CTGTGGCTG 1280
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                                                                                                                                                  Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 RP11-8J9 is from the library RPCI-11.1 constructed by Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNA sequence from clone
                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      requests: clonerequest@sanger.ac.uk
on Oct 2, 2001 this sequence version replaced g1:15591654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chapman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
This sequence is the entire insert of clone RP11-8J9 The true left end of clone RP4-732G19 is at 98457 in this sequence. The true right end of clone RP11-49P4 is at 37956 in this sequence.

Location/Qualifiers
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Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                            SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                     VECTOR: pBACe3.6
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298547.2 GI:15383894
HTG; 60S Acidic ribosomal protein P2; asparagine synthetase; calcium-dependent protein kinase; DNA polymerase delta; dual specificity protein phosphatase; guanine nucleotide-binding protein; PDZ domain; rat BRAIN-like protein; serine/threonine protein; PDZ domain; rat BRAIN-like protein; serine/threonine
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                                                                                                                         Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S., Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A., Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S., Suston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and
                                                                                                                                                                                                                                                        protein kinases; T-complex protein eta; T08A11.2-like protein domain; Y48E1C.2-like protein.
Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 116696)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFMAL3P3 116696 bp DNA linear IN Plasmodium falciparum MAL3P3, complete sequence. 298547 AL008977 AL0010164 AL139179 298548 298549 298550
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                                                                                                              Barrell, B.G
                                                        Nature 400 (6744),
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                                                                                             complete nucleotide sequence of
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/note="Sequence from overlapping clone RP4-732G19 (AL356793). Assembly confirmed by restriction digest." a 32904 c 32733 g 46543 t
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/clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Sequence from overlapping clone RP11-49P4
(AL136373). Assembly confirmed by restriction digest."
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/db_xref="taxon:9606"
/chromosome="1"
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54.3%;
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                                                        532-538 (1999)
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0.037;
                                                                                             chromosome
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AUTHORS
TITLE
JOURNAL
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6740. .
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For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. The following numbers may have changed slightly:
The true left end of clone MY434-3D7 is at 1 in this sequence. The true right end of clone MY549-3D7 is at 79511 in this sequence. The true right end of clone MY434-3D7 is at 114736 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (14-AUG-1997) P.falciparum Genome Sequencing Consortium,
Submitted (14-AUG-1997) P.falciparum Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On or before Aug 31, 2001 this sequence version gi:2894463, gi:2894495, gi:2894369, gi:2982521,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawson, D., Bowman, S. and Barrell, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mungall, K., Bowman, S., Churcher, C., Rajandream, M.-A. and Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="region duplicated in MAL3P2 to include the whole of PFC0235c in one entry, the whole CDS is in MAL3P2 and only the exons are shown in this entry to avoid duplicating the protein id"
/note="Match to PF00595 PDz, PDz domain (Also known or GLGF). Score 20.36" complement(join(9589. .16129,16327. .20041,20295. ./gene="PFC0335c, MAL3P3.3" .16129,16327. .20041,20295. .complement(join(9589. .16129,16327. .20041,20295. ./gene="PFC0335c, MAL3P3.3" hypothetical protein, note="PFC0335c, (MAL3P3.3), hypothetical protein, 3724 aa, predicted using hexexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNPTNNSIDNPTNNSIDNPTNNSIDNPTNNSIDNPINSPNYQQVTQSNIILEEENNTN
KTDIEKDIININFYSSEEKKIACEMIKOQIYYLLHSSMDKTFIETFNINIESHIYPSE
KRICVSYNMKSHTFKRSISNLSDLIEFSNKLKYVLDERIKKLYYEDKNNENAYLNKTL
RKELEIGKKERDVTNLSKKNLOMSIESSLKLIEKCMQNNYKONYEITLIBLIKLAYNML
PCKYYGFFLSNLCSTISTLSYYVNDLQGTFNFALKSIKYEPKYNVAMKCLGDAYRSFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="PFC0330w, MAL3P3.2"
/note="PFC0330w (MAL3P3.2), putative PDZ domain protei /note="PFC0330w (MAL3P3.2), putative PDZ domain (Also kn len: 700 aa, Match to PF00595 PDZ, PDZ domain (Also kn as DHR or GLGF). Score 20.36, predicted using hexExon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="part exon 3 of PFC0235c" complement(4520. .4587) /note="exon 2 of PFC0235c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4804. .4830)
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                                                                                                                                                                                                                                                                                                                                                                                                                 KFWQAKNFYDIAIYLGYKDEKGERFEDIVQELNNLTENALKNYDLLKEHMNNSTNIII
KKNIGIVLNKNPDSIGGCYVSYIIEGSKASKKNLHHGDQIVALNNHVTYGKPIDFCLK
AFQKNDGTYDIIFFKGNIIELYGLKAYKYLMKNDLFYALFENEQIVSFKRNETILFDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQR I NSKHNTFLYKNDTLNKLLNRKKNKHTLFYRSKKEKD I QESGYLY PFDHLEKKKT
KFPPDPY I PSEDEKESS I DI FHDK I NDDDLMI Y EDDDDAKKY FGKTTFNKPNI I QKDE
NSEDDQDDDLNDQNDDP I NNPTNNLTDNPTNNSTDNPTNNS I DNPTNNS I DNPTNNS I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative PDZ domain
/protein_id="CAB11102.1"
/db_xref="GI:3649753"
                                                                                                                                                                                                                                                                                                                                                                                   KGFGTFSEYGMSKAEFV"
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/chromosome="3"
                                                                                                                                                                                                                                                                                                       /gene="PFC0330w, MAL3P3.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MYLLMSKFLVWIIIFGNFFVVHFFLCFKIPNNKITNVLTYDNSK/
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                                                                                                                                                                                                                                                                     PDZ domain (Also known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein"
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gi:2665376,
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/product="hypothetical protein, /protein\_id="CAB11104.1" /db\_xref="GI:3649755"

NDINPLEHPDEQNQSLNKNKCLTGTNKKEKYMIPKGTEYQDKEKESSILTINQNDKKY

NDSEGKKYLNESSFENAFFELSDIWTPTINAYDYAHFLKSLFYRITYIEIKTKDGRII /translation-"MKEKEVDNLFPGDKDVTNLKQYFEGGDIKFENAELKKEREEIRK NKVFIECVQNIWMNILNKKMDDKFSKVEYFKIMLRICKVLIPQFDIKEIIKIVNDEWI

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TEKCIDIHDFDYVENKDVHDKIHEDRKEYCDESKLKYLPADDIKKMRSFIKINKKSKR
ENFLIISYMNEEIYFLIKKLKVEIIEPSIILNKNMHIEKQFLSPLGKYINDNLKEGKC
ISSKIIIDLMLEYMNTIISKNNGYVLYFNNYNILQHLDYFLHKLKGLSTIKYINYVHF
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KRKKKSQHFIDNLVKADKNEISENINKICDNNINNIYDESINNIYDESIN
                                                                                                                                                                                                                                                                                                                                                                              NKEDSYCNLLQFISIIEQEFQEKKYKNIIYIEYSNLWKMKCKITDDIEEKIKSYQKYN
RYKYNNKPAYFKGYNIYEKANYEQEIQFNNYCLVTYKKKQILLKCNIYDNYTICHNNS
FYLVNSYDDVISFEKNPTEYINVDDSSFKKLEQINNFDTYNNNNNNNIPIENEGFCLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IYKYDYKKKTNIDIKNFSINSIPIKNLLEKKYIYYLYREDIIYLENNINQINVYEQNN
HFNBFHIYDLLFQIIKPFNVFLNIIKILTIRYILHEHLQNCIITYNTFQHSIFNITDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAHIFEIHRIIEGKTISPLFIVRYICIHMKKIHQFNIYIIKEIIKSIIKLKHNFNLLI
MKKKNILINQCEIKKKMKRKKKMKKKKKKKIPEKKKLVNNEKKNLLFLFSSIMKIKFL
YNLIIIKQKNIKNVSFKNVLDKLSHIINIKDMAKDINLLLVLIEDMFFREKRKYLNKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FPYKYKGKRGKAKKGMLMINIKRKHEYDNLMKKKNGNEKTGNNNKKKNNKEDKNDYIN
NNNNNNNNNNDNNINVGYKRMONNINPNNLYEIKNNNFNLYHRYWSLFYKYCPVSYI
NDNKIIEGKKKFCVIYKNKIYMLNNHDYMIEFLKHPKFYASKKVKESVCFSLVIYFPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YFYCPVDIDNIVDIDTEFLILYNRYLFYFRTLEQINEFVKNPTFYLKQLKPNPSFVLP
FIFVYSCIEIENLHNELHKSTKCVVINREHLLSFGNKIKKYEKYIQTNNIDDNILMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLKYAFRVÞEYVIYLGCTSÞKKLLDRMKKVKNVEQIKNSEHTNHVTNSKGDGRKNFND
ASQEYRNKENQIKIPNIDKKNVDNNDKVEKDNLLDDIKKCSLKNKKIIEYLKKYSNIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNSY I NYYCPYVLKKHNWLYKS I DN I KLVYDEKVYYLSNLYHAF I FSKN I KYYQHNFN
I PPLRLLFLYDVPYKFNKD I KKNMYRKFFFKY I NLEKEC I IY I KYVF IYLLKY I FLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERESRORYIITGLPLHSKIFFYLKCMNISIDHVISFDIIKKEMNKDEENEDKGDGDDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDIQKKIIYLLETYEKLIHIDIGKYFKQYFFLSHQDKEQHKNNMKSNNNDDDVDNKIE
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EKDHLNNIEY IENLSEHLRHKYDIEMIPIDIVGNIRLYKLFYINMIKNNYSYYLKNNF
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                                                                                                                                                                                            YINLYDKILYSQTITNKTKQKKIKYT'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I I NNYNDKC I T NDMNYKQNYNHNNI NSPNDKDNI HMI NDEYKKKKY I NTSFTLLSKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y I D I EKY HSKS I KML I EKRLND I LRYRONLY HOLNMKRI DKI CAOFLRDNNY I KFSNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSLKYVIQKYRQKKYNKDHSSKQKEDIFKGSNQNELLTNEKDTGEKKQNLIHQDDHLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNDYKKKKYDIKIIPFDEDEKKSIYFYLNEIRKIINPYVHSYYNYNDILKNRICCKQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGDDFYGDEKESGKRNTNFKNLSQYYYNDKMNEEDTYELYKKYYSYNTYNDNIYHMNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y SNEYNESSDFTENCFAYNKDNINLAHLQKMFCKKY EKNILNSKY KFLENNLLNNIQK
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/gene="PFC0340w, MAL3P3.4"
                                                                                         /gene="PFC0340w, MAL3P3.4"
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Matches 183;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 AAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGT 126
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                                                                                                                                                                   TCGGTATAGTTCGATATTTTTTCAATTTATTTTTTTATAAAATAAAAAACTTACCCTAATTA 305
                                                                                                                                                                                                                                                                                   AATTTAATGCTTTATTAGTTTTAAACTTA-CTATATAAATTTTTCATATGTAAAATTTAA 245
                                                         TCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAAA 361
                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVKGIGMSNISLYVEBIIYSYIPKLDIPNCISNDDKFILFVSGLYINELNKSINNISL
LRNFILRLHGDTYLSENLIRLIILGNSLSNIDNDEKDMNTIDVFLSSLCSSIHIDLMP
GDKDPSDSNLPQQPFPNIFFKKARNFNSFQCVTNPYLFSIDNINICCMSGEPVHNITS
YSKNNKMNALKLIAQSRILSPTSPDTLGCYPFTKNDPFCLNDDNTYPHIFINGNCSKL
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/tanslatloo="mdekytnoeveelikhinenkknegehonkkikkkhfeyvnlse
r/translatloo="mdekytnoeveelikhinenkknegehonkkikkninndninnd
r/translatloo="mdekytnoeveelikhinenkknegehonkkkkninndninnd
ninndninnnoninndninndninnnnnynnyhiloylkelkynekoycigtifk
kmelrpsilneylseisilnninythdedilfledetarlklegninsdfyigdty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="PFC0345w, (MAL3P3.5), Hypothetical protein, len: 1712 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="PFC0345w, MAL3P3.5"
25880. .31015
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/protein_id="CAB11105.1"
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RESULT 13
AC087568
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DEFINITION REFERENCE SOURCE KEYWORDS /ERSION ACCESSION ORGANISM AUTHORS Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brook Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brook Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Ho,S.-C., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Masiello,C., Mastrian Pan troglodytes clone RP43-135M11, complete sequence. AC087568Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 150199) Pan troglodytes AC087568.2 AC087568 Pan troglodytes GI:16596569 150199 bp linear

PRI 02-NOV-2001

Mastrian, S.D.

Brooks, S.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y., Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Zhang,L.-H. and Green,E.D. D. NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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Similarity 48.7%;
GCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACTCCTAGTTGTTGT 432
                                           TAATAAAACTATATAAATATTTTATATTTATATTAATCTATAAATTATATTTATAT 38988
                                                                                                                                                                                             AGTTCGATATTTTTCAATTTATTTTTATAAAAATAAAAACTTACCCTAATTATCGGTAC 312
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Contact: nisc_mouse@nhgri.nih.gov
----- Project Information
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Center clone name: 135M11
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/db_xref="taxon:9598"
/clone="RP43-135M11"
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                                                                                              Sequence 321 from Patent Ax345250
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Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA
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Job time: 1538 secs
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Matches 176; Conservative
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/db_xref="taxon:32630"
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1. .5145
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Pred. No. 0.22;
0; Mismatches 159; Indels 4; Gaps
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Database :
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001a.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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Root cortex specif
                                                                                                                                  Root
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t cortex specific cortex specific cortex specific cortex specific an immune system metastasis a
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| Human metastasis a |          | 24 | 6095  | 12.4 | 6.   | 45         |   |
|--------------------|----------|----|-------|------|------|------------|---|
| Human immune syste | ABL3236  | 24 | 6095  |      | 56.6 | 44         |   |
| Chemically treated |          | 24 | 6095  | 12.4 | σ.   | 43         |   |
| Tumour suppressor  | AAS4631  | 22 | 6095  |      | σ.   | 42         |   |
|                    |          | 24 | 6013  |      | 6    | 41         |   |
| Human gene regulat |          | 24 | 6013  | •    | ٥.   | 40         |   |
| Drosophila melanog |          | 23 | 3296  | •    | 6    | 39         | O |
| Human chemically p |          | 24 | 16258 | •    | 57   | 38         |   |
| Chemically treated |          | 24 | 16258 | •    | 57   | 37         |   |
| Human immune syste |          | 24 | 10886 | 12.5 | 57   | 36         |   |
| Human DNA for stag |          | 24 | 8085  |      | 7.   | 35         | O |
| Tumour suppressor  |          | 22 | 8085  | •    | 7.   | 34         | O |
| Chemically treated | AAD22328 | 24 | 10279 | •    | 7.   | ω<br>ω     |   |
| Human immune syste |          | 24 | 10279 | •    | 57.6 | 32         |   |
| Chemically treated |          | 24 | 10279 | •    | 7.   | <u>3</u> 2 |   |
| Human immune syste |          | 24 | 6050  | •    | 7.   | 30         |   |
| Human DNA for stag | ABK33937 | 24 | 6050  | •    | .7   | 29         |   |
| Tumour suppressor  |          | 22 | 6050  | •    | 7.   | 28         |   |
| Human metastasis a |          | 24 | 8197  |      | 58   | 27         |   |
|                    |          | 24 | 8197  | •    | 58   | 26         |   |
|                    |          | 24 | 6062  | •    | 58   | 25         |   |
| Chemically pretrea | AAS63335 | 24 | 8842  | •    | œ    | 24         |   |
| _                  |          | 24 | 8842  |      | 58.2 | 23         |   |
| Human inflammatory |          | 22 | 700   | •    | œ    | 22         | O |
| Human breast cance |          | 22 | 422   | •    | 8    | 21         | a |
| Human prostate exp |          | 23 | 494   |      | ū    | 20         | a |
| Arachidonic acid m | AAC58017 | 21 | 20674 | •    | 59.4 | 19         |   |
| Human immune syste |          | 24 | 5407  |      | Ö    | 18         |   |
| Human secreted pro |          | 24 | 20420 | •    | 60   | 17         | O |
| Human immune/haema |          | 22 | 20420 | •    | 60   | 16         | O |
|                    | ABL3356  | 24 | 8305  | •    | 60   | 15         |   |
| Human immune syste |          | 24 | 5925  | •    | 60.2 | 14         |   |
| Human immune syste |          | 24 | 18997 | ٠    | 60.4 | 13         |   |
| Human DNA for stag |          | 24 | 18997 | •    | 60.4 | 12         |   |
| immune             | ABL33    | 24 | 6175  | 13.4 | σ    | 11         |   |
| Human immune syste |          | 24 | 8305  | •    | 66.4 | 10         | O |
|                    |          |    |       |      |      |            |   |

# ALIGNMENTS

RESULT 1 ABL58286 N. tabacum Nic gene product responsive element DNA sequence. 07-MAR-2002. Tobacco; plant; cis-acting element; transgenic; nicotine; Nic; NtQPT1; nitrosamine; responsive element; ds. 15-JUL-2002 ABL58286; ABL58286 standard; DNA; 456 BP. (UYNC-) UNIV NORTH CAROLINA STATE. 30-AUG-2000; 2000US-229198P. 28-AUG-2001; 2001WO-US26788. WO200218607-A2 Nicotiana tabacum. (first entry)

Obtaining plant with altered levels of desired protein regulated cis-acting element by introducing nucleic acid with the element operably linked to coding sequence of the protein to produce a not

WPI; 2002-371827/40.

Conkling MA,

Li Y;

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AAT5172
AAT5172
AAT5172
AAT6172
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AAT64
AAT6
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides a method of obtaining a plant with altered content of desired protein (P1) which is regulated by cis-acting element (E1). The method involves introducing exogenous nucleic acid (ENA) construct comprising E1 which is not operably linked to coding sequence or its complement of P1, into plant cell to produce transformed plant cell, where the cell contains ENA copies to alter level of P1 in plant regenerated from cells. The method is useful for obtaining a plant, preferably transgenic tobacco plant with altered content of P1, preferably a reduced amount of nicotine, which is regulated by E1 which is a Nic gene product, where altered content of P1 may be tobacco specific nitrosamines. The present sequence represents the N. tabacum Nic gene product responsive element DNA sequence.
                                                                                                                                                     Root cortex specific gene TobRD2 promoter (dell.0).
                                                                                                                                                                                           15-OCT-1997
                                                                                                                                                                                                                                                                       AAT51750
                     WO9705261-A1
                                                         Nicotiana tabacum
                                                                                             Root cortex-specific
Insecticide; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 BP; 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; 57 C;
                                                                                                               promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
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                                                                                                               TobRD2;
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                                                                                           2; tobacco;
biological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1030 BP; 388
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                                                                  CCTAGTTGTTGTTATAGGTAAAAAGCAGTTACAGAG
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Pred. No. 4e-68;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 T;
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Best Local Similarity
Matches 456; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated DNA (AAT51749), designated del1.3, comprises a 1294 by 5'-deletion mutant of the tobacco RD2 gene (TobRD2) promoter (see also AAT51746), which directs root cortex-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA directing heterologous gene expression in the root cortex - used e.g. for expressing insecticidal Bacillus proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1294 BP; 515 A; 174 C; 203 G; 402 T; 0 other;
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AATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACT 420
                                                                    AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAAACCTAAA 360
                                                                                                                                                                 TTTAATCGGTATAGTTCGATATTTTTTCAATTTTTTTATAAAATAAAAAACTTACCCT 300
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Bacillus thuringiensis; biological control; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Pred. No. 4e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1372 BP; 532 A; 187 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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ATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCC
                                                                                                             ATTAGTATTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCC
                                                                                                                                                                                                                           GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA
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100.0%; F
tive 0;
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Pred. No. 3.9e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 G; 438 T; 0 other;
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RESULT 5
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                                                                                                                   Query Match
Best Local S
Matches 456
                                                                                                                                                                                                                An isolated DNA (AAT51747), designated del2.0, comprises a 1988 bp portion of the tobacco RD2 gene (TobRD2) promoter (see also AAT51746), which directs root cortex-specific expression of associated genes: Del2.0 and truncated TobRD2 promoters (see also AAT51748-56) can be used in DNA cassettes to direct the expression of heterologous genes in the root cortex layer of transgenic monocot or dicot plants, e.g. to express Bocillus thuringiensis crystal proteins in tobacco for the control of root-damaging pests. Del2.0 directed high levels of GUS reporter gene expression (4-fold higher than the CaMV35S promoter) in transgenic tobacco root cortex.
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 33-34; 53pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-145698/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum.
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                                                    959
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                   61
                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      cting heterologous gene expression in the root cortex expressing insecticidal Bacillus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA;
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specific
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Pred. No. 3.8e-68;
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An isolated DNA (AAT51746) comprises the tobacco RD2 gene (TobRD2) promoter, which directs root cortex-specific pression of associated genes. A clone containing the isolated DNA was obtd. from a tobacco seedling genomic library by screening with TobRD2
                                                                                                                                                                    DNA directing heterologous gene expression in the root cortex e.g. for expressing insecticidal Bacillus proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            that TobRD2 mRNA is expressed only in the cortex layer of roots. Truncations of the promoter region (see also AAT51747-54) were prepd. by PCR. The full-length or truncated promoters can be used in DNA cassettes to direct root cortex-specific expression of heterologous genes in transgenic monocot or dicot plants, e.g. to express Bacillus thuringiensis crystal proteins in tobacco for the control of root-damaging pests.
Conkling MA,
                                                                                                                                                                                              AAT51751
                                                                                  W09705261-A1
                                                                                                   Nicotiana tabacum
                                                                                                                 Root cortex-specific promoter; TobRD2; tobacco; transgenic insecticide; Bacillus thuringiensis; biological control; ss
                                                                                                                                          Root cortex specific gene TobRD2 promoter (del0.7).
                                                                                                                                                             15-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2010 BP; 729 A; 276 C; 303
                                  28-JUL-1995;
                                                 24-JUL-1996;
                                                                  13-FEB-1997
                 (UYNC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                        1319
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                                                                                                                                                                                                                                                                                        361
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                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTT
                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                              CCTAGTTGTTGTTATAGGTAAAAAGCAGTTACAGAG
                                                                                                                                                                                                                                                                                AATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACT
                                                                                                                                                                                                                                                                                                                                                                       GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTT
                                                                                                                                                                                                                                       CCTAGTTGTTATAGGTAAAAGCAGTTACAGAG
                                                                                                                                                                                                                                                                       AATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACT
                                                                                                                                                                                                                                                                                                       AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAA
                                                                                                                                                                                                                                                                                                                 AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAAAACCTAAA
                                                                                                                                                                                                                                                                                                                                       TTTAATCGGTATAGTTCGATATTTTTCAATTTATTATAAAATAAAAAACTTACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
               NORTH CAROLINA STATE
                                                                                                                                                            (first
Mendu N,
                                  95US-0508786
                                                 96WO-US12158
                                                                                                                                                                                             DNA;
                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.9%;
                                                                                                                                                                                              722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 451.2; 1
Pred. No. 2.4e
0; Mismatches
                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4e-67;
3;
                                                                                                                                                                                                                                      1414
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                                                                                                                         plant;
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ABL32348
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WPI; 2002-130909/17
               Olek A,
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Query Match
Best Local S
Matches 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 38; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA directing heterologous gene expression in the root cortex - used e\cdot g\cdot for expressing insecticidal Bacillus proteins
                                                                                                                                                                                                                                                                                                                                                              Sequence 722 BP; 278
                                                                                                                                                                                                                                                                                                                                                                                                        root cortex.
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                                        429
121
                                                                                                                             369 CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACTCCTAGTTG
                                                                                                                                                                                                                       309 GTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAAAATCGGTT
                                                                                     61
                                                                                                                                                                                                                                                                      148;
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                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                          TTGTTATAGGTAAAAAAGCAGTTACAGAG 456
                                                                                  CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACTCCTAGTTG
TTGTTATAGGTAAAAAGCAGTTACAGAG
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                         32.5%;
                                                                                                                                                                                                                                                                                                                                                           A; 107 C; 129
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                                                                                                                                                                                                                                                                    Score 148; DB; Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                           G; 208 T;
148
                                                                                                                                                                                                                                                                                         DB 18;
1.5e-16;
                                                                                                                                                                                                                                                                                                                                                           0 other;
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                                                                                     120
                                                                                                                               428
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gene;
                                                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antisporiatic; antiarthritic; antidiabetic; anticorosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                        30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                       03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                          02-JUL-2001; 2001WO-EP07537
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                                            (EPIG-)
                                                                                                                                                                                                                                                                                             sapiens.
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                                              EPIGENOMICS
Piepenbrock C,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
         06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune syst genes which are modified by the methylation of cytosines. The can be used in the diagnosis and treatment of immune system can be used in the diagnosis and treatment.
                                                                                                                                                                                            Human metastasis associated
                                                                                                                                                                                                                                                                ABL34464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                             cytosine
                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                          ABL34464;
                                                                   06-APR-2001;
                                                                                           18-OCT-2001.
                                                                                                               WO200177376-A2
                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 321; 32pp +
                                                                                                                                                          is associated
methylation;
                                                                                                                                                                                                                                                               standard; DNA; 5145
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATAAAGATACTTGAAATAGCTTAGTTTAAATATAATAGCATAATAGATTTTAGGAATT
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         2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                   (first entry)
                                                                    2001WO-EP03970
                                            2000DE-1019058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.6%;
                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      provides a number of human immune system associated
                                                                                                                                                            cytostatic; ds.
                                                                                                                                                                                            gene SEQ
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                                                                                                                                                                                                                                                                ВP
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                                                                                                                                                                     gene therapy;
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                                                                                                                                                                                                                                                                                                                         845
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                                                                                                                                                                        cancer;
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WO200200928-A2

sapiens

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RESULT 10
ABL33568/c
ID ABL335
XX ABL335
XX ABL335
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XX Human;
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Best Local :
                                                                                   antirheumatic; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilanonneurofibromatosis; rheumatoid arthritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for diagnosis of cancers by analysis of cy also for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of human metastasis associated genes which are modified by cytosine methylation. The sequences can be used in the diagnosis and treatment of cancer. The present sequence is one of the genes of the invention.
                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek A,
                                                                                                                                                                                          Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5145 BP; 1470 A; 27 C; 855 G; 2793 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 17;
                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                         ABL33568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                 TATCGGTACAGTTATAGATTTATATAAAAATCTACGGTT 342
                                                                                                                                                                                                                                                                                                                                                                                       AATCGGTATAGTTCGATATTTTTCAATTTTTTTATAAAATAAAAAACTTACCCTAAT
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                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methylation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5145;
                                                                                                disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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Query Match
Best Local 9
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      antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising for diagnosis and treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8305 BP; 2181 A; 185 C; 1901 G; 4038 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated system which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-)
                                                  Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                     Human immune
                                                                                        26-MAR-2002
                                                                                                             ABL33307;
                                                                                                                                 ABL33307 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis
                                                                                                                                                                                                                                                                                                                                                                                              6424
                                                                                                                                                                                                                                                                                                            6304
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                     TATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1541; 32pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock
                                                                                                                                                                                   GGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAAAAT 363
                                                                                                                                                                                                                                                                                                                                                                        AAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGTA 127
                                                                                                                                                                                                                            GGTATAGTTCGATATTTTTCAATTTATTTTATAAAATAAAAAACTTACCCTAATTATC
                                                                                                                                                                                                                                                                                       ATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAATC
                                                                                                                                                                                                                                                                                                             TTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGAAAA 187
                                                                                                                                                                                                                                                                     Conservative
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2000DE-1043826
                                                                    system associated gene SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rising fragment of chemically modified treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%;
                                                                                        entry)
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                                                                                                                                  6175
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66.4; DB 2
Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24;
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                     181;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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abnormal
          anaemia;
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                                                 RESULT 12
ABK33948
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18-JUN-2002 ABK33948; ABK33948

(first entry)

DNA;

ВP

4854

4794

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Query Match
Best Local S
Matches 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01ek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising frag
for diagnosis and treatment
cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6175 BP; 1506 A; 154 C; 1357 G; 3158 T; 0 other;
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                                                                              4855
187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                             ATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTTGTGCCTTGCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piepenbrock
                                                                                                                                                                                                                                                                          ATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCCATGAAA 186
                                                                                                                                                                                                                                                                                                                      AAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGT
                                       CGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCA
                                                                              ATTTATTTATGTTTATATTTATTTATATTTATATGTATATTTATATTTATATTTAAT
                                                                                                                   AATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAAT 246
                                                                                                                                                                                                                                       13.4%;
nilarity 48.7%;
Conservative
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2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment of chemically modified nent of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61; DB 2
Pred. No. 0.046
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6175;
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δõ

밁 Ş B Ş В Ş

밁 20 밁 Ş B Human

DNA for staging of Astrocytomas #16.

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Sequence 18997
BP;
4675
P
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4016 G;
10007 T;
0 other;
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The present invention provides a number of human immune system associated

CC complement. Also included are an oligonucleotide or peptide nucleic (I), probes for detecting cytosine methylation or single-cc nucleotide polymorphisms (SNP) in (I), an array of oligoners (I), probes for detecting cytosine methylation or single-cc nucleotide polymorphisms (SNP) in (I), an array of oligoners (I), converting the peptide nucleic acids for analysing diseases associated with the cmethylation states of the CpG dinucleotides of (I). The array is useful cf or determining genetic and/or epigenetic parameters, classification, cd differentiation, grading, staging, treatment and/or diagnosis of astrocytomas, or the predisposition to astrocytomas by analysing containing a biological sample containing genomic CDNA, extracting the genomic DNA, converting cytosine bases which are cumethylations, involves obtaining a biological sample containing genomic CDNA, extracting the genomic DNA, in the genomic DNA sample, to uracil or another base which is dissimilar to cytosine in terms of hybridisation behaviour, by chemical treatment and amplifying chemically pre-treated CC amplificates carry a detectable label. The method further involves and complete the correct of the cytosine positions by reference to CC analysing methylation status of one or more cytosine positions, and CC analysing methylation status of the cytosine positions by reference to CC one or more data sets. The genomic DNA is chemically treated by using a CC brain tissue, based on the specific genomic DNA it emplification or the amplificates are detected in a mass spectrometer. The amplification or complete course and complete course of the course of the analysing a typical mass course and course detectable molecule fragments having a typical mass course detected by matrix assisted laser desorption/ionization mass spectrometer. CC (MALDI) or using electron spray mass spectrometer y (ESI). The course of the invention.

CC Malding of the chemically pre-treated eference DNA cc samples of the chemically pre-treated eference DNA cc samples of the chemi of the printed specification, but format directly from WIPO at The invention relates to a nucleic acid comprising a sequence (least 18 bases in length of a segment of chemically pre-treated DNA which has any one of the sequences of (ABK33919-ABK34032) or the sequences Novel chemically modified genomic DNA sequences, useful in the characterisation, classification, differentiation, grading, staging, characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to Note: The sequence data for this patent did not form part Claim 1; SEQ ID No 31; 37pp; English. Olek A, 30-JUN-2000; 01-SEP-2000; 02-JUL-2001; 2001WO-EP07538. Homo sapiens. matrix assisted bisulphite; Human; ds; astrocytoma; (EPIG-) EPIGENOMICS AG. ftp.wipo.int/pub/published\_pct\_sequences LO-JAN-2002 Piepenbrock C, brain tissue; 2000DE-1032529 2000DE-1043826 ln tissue; MALDI; ESI; electron spray mass spectrometry;
laser desorption/ionization mass spectrometry. cytostatic; staging; cysteine methylation; e; MALDI; ESI; electron spray mass spectrom Berlin was obtained 'n electronic ဝှ (I) of genomic CpG;

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RESULT 13
ABL32570
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Matches
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Claim 1; SEQ ID NO 543; 32pp + Sequence Listing; German
                                                         Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antifheumatic; antiathritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anae acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                       cytosine methylation
                                                                                                                     WPI; 2002-130909/17.
                                                                                                                                                            Olek A,
                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                          30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL32570 standard; DNA; 18997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurofibromatosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 TTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATAAAGATACTTGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATTTATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTATTAATAGTTTTTTATTTTTTAGATTTTTTTTAGATTTTAAATTGAAATGATAAG
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2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system associated gene SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antianaemic; cytostatic;
                                                                                                                                                            Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   psoriasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bowel disease,
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                                                           gene, useful
abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18997 BP; 4675 A; 299 C; 4016 G; 10007 T; 0 other;
                                                                                                                                                                                                                                                            neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antifheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arterioscierosis; ana acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy
          Olek A,
                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation;
antiarteriosclerotic; antianaemic; cytostatic; nooti
                                                                                                                                                                                                                                                                                                                                                                    Human immune
                                                                                                                                                                                                                                                                                                                                                                                                                              ABL33576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL33576 standard; DNA;
                                                                                                                                            03-JAN-2002
                                                                                                                                                                          WO200200928-A2
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                  gene;
                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                      30-JUN-2000;
01-SEP-2000;
                                                                                                                02-JUL-2001;
                                                                                                                                                                                                                                                   neurofibromatosis; rheumatoid
                                         (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATTTGTTTT 13824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTTTTTTTTTTTTTATATTTTTTAAAAATTTAATATCGTGTTTTTTTATTTTAATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCCATGAAAAATTTAATGCTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGTATTTTGAGTTTA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGATTTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATTTTTTCAATTTATTTTATAAAATAAAAACTTACCCTAATTATCGGTACAGTTAT
            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                  system associated gene SEQ ID NO: 1549
                                                                                                                  2001WO-EP07537.
                                                                       2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.2%;
49.7%;
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             Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                  arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No. 0.053;
                                                                                                                                                                                                                                                                               arteriosclerosis; anaemia;
                                                                                                                                                                                                                                                  ease; AIDS; epilepsy;
psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156;
                                                                                                                                                                                                                                                                                                                        nootropic;
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RESULT 15 ABL33569

ABL33569 standard;

DNA;

8305

ВP

gene;

ds.

30-JUN-2000; 01-SEP-2000;

2000DE-1032529 2000DE-1043826 2001WO-EP07537

02-JUL-2001;

WO200200928-A2 Homo sapiens. neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anacacute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; arteriosclerosis; anacacute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; arteriosclerosis; anacacute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; arteriosclerosis; anacacute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; arteriosclerosis; anacacute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; arteriosclerosis; anacacute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; arteriosclerosis; anacacute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; arteriosclerosis; anacacute myeloid leukaemia; Alzheimer's disease; arteriosclerosis; anacacute myeloid leukaemia; arteriosclerosis; anacacute myeloid leukaemia; arteriosclerosis; arteriosclerosis; anacacute myeloid leukaemia; arteriosclerosis; arteriosc

epilepsy;

anaemia; disease;

Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic;

Human immune system associated

gene SEQ ID NO:

1542.

26-MAR-2002 ABL33569;

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1549; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5925 BP; 1510 A; 105 C; 1246 G; 3064 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention provides a number of human immune system associated es which are modified by the methylation of cytosines. The sequences be used in the diagnosis and treatment of immune system disorders,
 2439
                                                                    2379
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                                                                                                                                    2319
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                                                                                                                                                                  AAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTA
                                                                                                                                                                                                   GAATTTTGAATTTGTTTTTTAGTTTAGGTTTGATATTATATATAGATTTGATTTGTTTTA
                                                                                                                                                                                                                                  GTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGA
                                                                                                                                                                                                                                                                    ATAAGGGATTTTTAGATATAATATTTATATTTAAATTTTAAATGTATGTTTTTAAGAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methylation
                                                                                                                                 GTATTTTTTGTTGTAGTAAATTAAAATTTAATGGGTTTT
                               ATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTT 345
                                                                  ATCGGTATAGTTCGATATTTTTCAATTTATTTTTATAAAATAAAAACTTACCCTAATT
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                    13.2%;
                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                        138;
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                                                                                                                                                                                                                                                                                                                                                                         5925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acute myeloid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful
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184 2258

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Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8305 BP; 2163 A; 185 C; 2060 G; 3897 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1542; 32pp + Sequence Listing; German.
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                                                                                                                            2062
188
                                       308 GGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAAAAT 363
                                                                                                                                                                                   248 GGTATAGTTCGATATTTTTCAATTTATTTTTTATAAAATAAAAACTTACCCTAATTATC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                        128 TTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGAAAA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGTA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 TATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATA 67
                                                                                                                                                                                                                                                 ATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAATC 247
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nilarity 48.0%;
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Pred. No. 0.066;
0; Mismatches 185; Indels
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Search completed: June 9, 2003, 07:16:39
Job time: 192 secs

2, Appli 1, Appli 13, Appl 13, Appl 534, Appl 534, Appl 287, Appl 13, Appli 11, Appli

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Total number of hits satisfying chosen parameters:
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-508-786-5
PCT-US96-12158-4
US-08-508-786-3
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PCT-US96-12158-3
US-08-508-786-1
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US-08-508-786-1
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US-08-98-416-138
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Sequence
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                                                                                                  ;; TYPE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (ger
US-08-508-786-5
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US-08-508-786-5
                                                                                                                                                            CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEPAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 base pairs
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                                                 Query Match
Best Local S
Matches 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Conkli
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Conkling, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Charlotte
STATE: No. 5837876th Carolina
COUNTRY: USA
ZIP: 28234
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  456;
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post Office Drawer 34009
                                                   Conservative
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                                                                                                               DNA (genomic)
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US-08-446-855A-1
US-08-150-741-1
US-08-487-8268-13
US-08-98-416-837
US-08-998-416-837
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US-09-004-8382-1
US-09-004-8382-1
US-09-904-846-1137
US-08-998-416-1137
                                                 0;
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                                               Score 456; DB 2;
Pred. No. 5.5e-85;
Mismatches 0;
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Result No.

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Issued\_Patents\_NA:\*
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2: /cgn2\_6/ptodata/1,
3: /cgn2\_6/ptodata/1,
4: /cgn2\_6/ptodata/1,
5: /cgn2\_6/ptodata/1,
6: /cgn2\_6/ptodata/1,

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Gapext 1.0

Title: Perfect score:

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GENERAL INFORMATION:
    Query Match
                                                                                                                                                                                            APPLICATION NUMBER: PCT/US96/
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
                                                                                                                      TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                  TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mendu, Nar
APPLICANT: Song, Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Conkling, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
ZIP: 282
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Post Off
CITY: Charlotte
STATE: North Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTLE OF INVENTION:
                                                                                    TYPE: nucleic acid
                                                              TOPOLOGY:
                                                                         STRANDEDNESS:
                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Gibson
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                                                                                                                                                                                                                                                                                                                                                                                                                         North Carolina
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                                                                                                                                                  919-881-3175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 456; Conserv
                                TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
                                                            CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Root Cortex Specific Gene Promoter NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             STREET: Post Office Drawer 34 CITY: Charlotte STATE: No. 5837876th Carolina
                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Gibson
STREET: Post Office Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park &
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1294 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mendu, ...
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Mendu, Nandini
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                                                                                                    5051-294
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                                                                                                                                                                                                                                     Version #1.30
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                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application PC/TUS9612158
GENERAL INFORMATION:
APPLICANT: Conkling, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Sin
Matches 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
FILING DATE OF THE PROPERTY AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,66
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
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                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                           ADDRESSEE: Kenneth D. Sibley; Bell, ADDRESSEE: Gibson
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ER: 5051-294
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Pred. No. 5.6e-85;
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Best Local Similarity
Matches 456; Conserv
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TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Pred. No. 5.6e-85;
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US-08-508-786-3
US-08-508-786-3
; Sequence 3, Application US/08508786
; Patent No. 5837876
; GENERAL INFORMATION:
 APPLICANT: Conkling, Mark A.
 APPLICANT: Mendu, Nandini
 APPLICANT: Song, Wen
 TITLE OF INVENTION: Root Cortex Specific Gene Promoter
 INUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park &
 ADDRESSEE: Gibson
 STREET: Post Office Drawer 34009
 CITY: Charlotte
 STATE: No. 5837876th Carolina
 COUNTRY: USA
 ZIP: 28234
COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

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RESULT 6
PCT-US96-12158-3
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                                                                                                                                                                                                              Sequence 3, Application PC/TUS9612158 GENERAL INFORMATION:
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                                                                                        APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promoter
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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LENGTH: 1372 base pair
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                           ADDRESSEE: Kenneth D.
ADDRESSEE: Gibson
STREET: Post Office Dr
CITY: Charlotte
STATE: North Carolina
                                                                                                                                                                                           APPLICANT: Conkling, Mark A.
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REFERENCE/DOCKET NUMBER: 50
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                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                             Post Office Drawer 34009
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Pred. No. 5.6e-85;
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RESULT 7
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TELEPHONE: 919-420-2200
TELEPAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1372 base pairs
                                           Sequence 2, Application US/08508786
Patent No. 5837876
GENERAL INFORMATION:
APPLICANT: Conkling, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
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NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
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CORRESPONDENCE ADDRESS:
             NUMBER OF SEQUENCES:
                                 TITLE OF INVENTION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 100.0%;
Local Similarity 100.0%;
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Pred. No. 5.6e-85;
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                                              RESULT 8
PCT-US96-12158-2
Sequence 2, Application PC/TUS9612158 GENERAL INFORMATION:
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TELEPHONE: 919-420-2200
TELEPAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1988 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 5.8e-85;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1988 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 11near
MOLECULE TYPE: DNA (genomic
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Best Local Similarity
Matches 456; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS: Renneth D. Sibley; Bell, Seltzer, Park & RADRESSEE: Kenneth D. Sibley; B
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TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
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NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 50
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STATE: North Car
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    CCTAGTTGTTGTTATAGGTAAAAAGCAGTTACAGAG 456
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ilarity 100.0%;
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Song, Wen
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Mendu, Nandini
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Pred. No. 5.8e-85;
Pred. No. 5.8e-85;
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31.665 REFERENCE/DOCKET NUMBER: 50. TELECOMMUNICATION INFORMATION: TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,786
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LENGTH: 2010 base pairs
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MEDIUM TYPE: Floppy
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NUMBER OF SEQUENCES:
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APPLICANT: Mendu,
APPLICANT: Song, V
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CITY: Charlotte
STATE: No. 58378
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                                                                              TTTAATCGGTATAGTTCGATATTTTTTCAATTTATTTTTTATAAAATAAAAAACTTACCCT 300
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Pred. No. 5.8e-85;
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NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
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MEDIUM TYPE: Floppy
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APPLICANT: Song, Wen
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: North Carolina
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                                                                                                                                           Matches 148;
                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 722 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 50:
TELECOMMUNICATION INFORMATION: 919-420-2200
TELEPHONE: 919-881-3175
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FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: 11
                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,665
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Mendu, Nandini
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                                                                                                                                                       32.5%; Score 148; DB 2; 100.0%; Pred. No. 2.6e-22;
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PCT-US96-12158-6
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                                                                                                                              RESULT 13
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GENERAL INFORMATION:
                                                                                      Patent No.
                                                                                                 Sequence 288,
                                                                                                                                                                                                                                                                                                                                         Matches 148;
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TOPOLOGY: 11
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Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 base pairs
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NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,
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NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mendu, Nai
APPLICANT: Song, Wen
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Kennetl
ADDRESSEE: Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 GTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAGCCTAAAAATCGGTT
                                                                                                                                                                                                                                                                                         121 TTGTTATAGGTAAAAAGCAGTTACAGAG 148
                                                                                                                                                                                                                                                                                                                              429 TTGTTATAGGTAAAAAGCAGTTACAGAG 456
                                                                                                                                                                                                                                                                                                                                                                                                            369 CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACTCCTAGTTG 428
                                                                                                                                                                                                                                                                                                                                                                    GTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAAAATCGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application PC/TUS9612158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 North Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post Office Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                722 base pairs
                                                                                                                                                                                      Application US/08998416
Wendland, Jurgen
Knechtle, Philipp
Rebischung, Corinne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conkling, Mark A.
                                                                               Pohlmann, Rainer
Steiner, Sabine
                                                                 Mohr, Christine
                                                                                                                           Philippsen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kenneth D. Sibley; Bell, Seltzer, Park &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nandini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.5%; Score 148; DB 5; 100.0%; Pred. No. 2.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US96/12158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Gaps

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RESULT 14
US-09-641-638-651
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INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
SEQUENCE 837 base pairs
FRUCTH: 837 base pairs
         Sequence 651, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: PAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 168; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                             302
                                                                                                                                                                                                                                                                                             182 TGAAAAATTTAATGCTTTATTAGTTTTTAAACTTACTATATAAATTTTTCATATGTAAAAT 241
                                                                                                                                                                                                                                                                                                                                                         354
                                                                                                                                                                                                                                                                                                                                                                                   124 AGTATTTTGAGTTTAATTACTTATTG--ACTTGTAACAGTTTTTATAATTCCAAGGCCCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                         4 AACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27709
                                                                                                                   TTTATTTATTTAATTAAATTAATTA 562
                                                                                                                                                                                                                                                                       TAAATATTATGTTGATTTATATTATTTAATCTTTTTATAAGAATTATTATTAAAAATTAAT
                                                                                                                                                                                                                                                                                                                                                 AATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATTAGTTATTAAAATATTATTAGATATTATTATTTTCTTTAATAAATTATTAAATAGA 293
                                                                                                                                                         ATTATCGGTACAGTTATAGATTTATATAA. 330
                                                                                                                                                                                                                               TTAATCGGTATAGTTCGATATTTTTCAATTTATTTTATAAAATAAAAAAACTTACCCTA 301
                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CH 0016/97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 60.6; DB 4;
Pred. No. 0.00016;
0; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 837;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                       473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERRUCE: GENEST OSICP1

CURRENT APPLICATION NUMBER: US/09/641,638

CURRENT FILING DATE: 2000-08-16

PRIOR APPLICATION NUMBER: US 09/502,330

PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                             LOCATION: 16775..16945
OTHER INFORMATION: exon 13
                                                                                                                                                                 LOCATION: 16567..16667
OTHER INFORMATION: exon
                                                       LOCATION: 17063..17554
OTHER INFORMATION: exon
                                                                                                                                                                                                             NAME/KEY: exon
                                                                                                                                                                                                                           OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                     OTHER INFORMATION: exon 10
                                                                                                                                                                                                                                                                                                                           LOCATION: 12254..12340
OTHER INFORMATION: exon
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 6349..6509
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                 NAME/KEY: misc_feature
OCATION: 17555..20674
                                                                                                                                                     NAME/KEY: exon
                                                                                                                                                                                                                                                                 NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
OCATION: 7379..7522
                                                                                                                                                                                                                                                   OCATION: 13308..13429
                                                                                                                                                                                                                                                                                                                                                                                                   OCATION: 8645..8854
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1123..3123
                                                                                                                                                                                                                                                                                                         OCATION: 12854..13023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AME/KEY: exon
OCATION: 3871..4072
                                                                                                                                                                                                                                                                                                                                                                                     AME/KEY: exon
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OCATION: 5996.
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OCATION: 5552..5633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HER INFORMATION: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20674
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Chumakov, Ilya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blumenfeld, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . . 6099
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3'regulatory region
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OTHER INFORMATION: 10-346-141:
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263:
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305:
NAME/KEY: allele
LOCATION: 6338
OTHER INFORMATION: 10-347-74:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 4109
OTHER INFORMATION: 10-343-278 :
NAME/KBY: allelle
LOCATION: 4170
OTHER INFORMATION: 10-343-339 :
NAME/KBY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 :
NAME/KBY: Allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 10-508-245 NAME/KEY: allele LOCATION: 1559 OTHER INFORMATION: 10-509-284 NAME/KEY: allele LOCATION: 1570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
OCCATION: 2832
THER INFORMATION: 10-513-250 : po
TAME/KEY: allele
OCATION: 2844
OCATION: 2844
THER INFORMATION: 10-513-262 : po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOCATION: 2323

WHER INFORMATION: 10-511-337 :
IAME/KEY: allele
JOCATION: 2341

WHER INFORMATION: 10-512-36 :
IAME/KEY: allele
JOCATION: 2623

JOCATION: 2623

JOCATION: 2623

JOCATION: 2623

JOCATION: 2623

JOCATION: 2623
                                                                   AME/KEY: allele
OCATION: 6375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HER INFORMATION: 10-343-231 : deletion of CUME/KEY: allele CATION: 4088
HER INFORMATION: 12-206-366 : polymorphic better Information: 12-206-366 : polymorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HER INFORMATION: 10-510-173
ME/KEY: allele
CATION: 2048
HER INFORMATION: 10-511-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ME/KEY: allele
CARTION: 2934
HER INFORMATION: 10-513-352 : polymorphic base A or
ME/KEY: allele
CARTION: 2947
CARTION: 2947
CARTION: 10-513-365 : polymorphic base A or
ME/KEY: allele
CARTION: 3802
CARTION: 3802
CARTION: 12-206-81 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ME/KEY: allele
CATION: 4062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E/KEY: allele
ATION: 1827
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TION: 1182
INFORMATION: 10-347-111 : polymorphic base G or KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : polymorphic base G or
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| 04<br>04<br>05<br>05   | A X B C  |                             |   |   |                           |                      |                           |   |   |  |   |  |
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| 111 GATTTTAG 11124 TTAAAATT 171 TCCAAGGC 11184 AATTTAAA 231 ATATGTAA   | Utery Match Best Local Similarity 49. Best Local Similarity 49. Best Local Similarity 49. Conservative Similarity 59. Find Conservative Fi |                             | OTHER INFORMATION: OTHER INFORMATION: 07HER INFORMATION: 07HER INFORMATION: | OTHER INFORMATION: NAME/KEY: allele LOCATION: 12429 OTHER INFORMATION: NAME/KEY: allele |                           | ION:                 |                           | LOCATION: 8658 OTHER INFORMATION: NAME/KEY: allele LOCATION: 8658 | OTHER INFORMATION: NAME/KEY: allele LOCATION: 7668 OTHER INFORMATION: | NAME/KEY: allele LOCATION: 6534 OTHER INFORMATION: NAME/KEY: allele LOCATION: 6611 | R INF   | LOCATION: 6429 OTHER INFORMATION: NAME/KEY: allele |
| GGAATTAGTAT  | Y 49.5%;<br>EVATIVE<br>TITGCIAATAA<br>               <br>  TAGCIAAGGA  | 10-507-35                   | 10-507-17   | 10-350-72   | 36                        | 10-349-216           | 10-349-97                 | 0-349-4   | 10-347-341  | 10-347-27  | 10-347-203  | 10-347-165   |
| GATTTTAGGAATTAGTATTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAAAT  TTAAAATTAAAATTTAAATTTAAATTAAAATTTAAAATTTAAACTTATTA | AGATACTTTAATATTTAATTAATTAATTAAATTT   | 3 : polymorphic base C or T | 70 : polymorphic base A or G<br>21 : polymorphic base A or C                | 2 : polymorphic base C or T  32 : polymorphic base C or T                               | 8 : polymorphic base C or | .6 : deletion of CTG | : polymorphic base A or G | : polymorphic base C or   | <pre>8 : polymorphic base A or G 1 : polymorphic base A or G</pre>    | 1 : polymorphic base A or T  | <ul><li>3 : polymorphic base A or G</li><li>0 : polymorphic base A or G</li></ul> | 5 : polymorphic base C or T                        |
| 7 170 A 11183 C 230 T 11243 A 290 A 11303  |  |                             |   |   |                           |                      |                           |   |   |  |   |  |

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11304

AACTTACCCTAATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAA 350

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; MOLECULE TYPE: [
; ORIGINAL SOURCE:
; ORGANISM: PAG1
US-08-998-416-1137
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US-08-998-416-1137
                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1137, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 919-541-8689
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GETTITLE OF INVENTION: ANNUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGISTRATION NUMBER:
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148;
                   64 AATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATT 123
                                                                                                      4 AACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSER: No. 6239264artis Corporation
T: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
                                                                      AAATTAGTTATTAAAATATTATTAGATATTATTATTTTCTTTAATAAATTATTAAATAGA
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                                                                                                                                                Conservative
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TENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TENTION: AND USES THEREOF
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Knechtle, Philipp
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Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mohr, Christine
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                                                                                                                                                                                                                                          PAG1692RP
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Search completed: June 9, 2003, 08:04:35 Job time: 46 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         June
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456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_NA:*
                    /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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Copyright (c) 1993 - 2003 Compuç
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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5105.512 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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|--------|-------|---------------------|--------------------------|----|---------------------|---------------------|--|
| c<br>L | 58.2  | 12.8                | 858                      | 9  | US-10-198-846-7035  | Sequence 7035, Ap   |  |
| N      | 57    | 12.5                | 53332                    | ဖ  | US-10-224-562-3     | Sequence 3, Appli   |  |
| w      | 57    | 12.5                | 53332                    | 10 | US-09-801-861-3     | Sequence 3, Appli   |  |
| c 4    | 54.4  | 11.9                | 6327                     | 9  | US-10-239-676-151   | Sequence 151, App   |  |
| Ŋ      | 53.6  | 11.8                | 14078                    | 7  | US-08-781-986A-191  | Sequence 191, App   |  |
| ი<br>6 | 53.6  | 11.8                | 513509                   | 9  | US-09-754-853A-4    | Sequence 4, Appli   |  |
| c 7    | 53.4  | 11.7                | 272                      | 10 | us-09-969-373-607   | Sequence 607, App   |  |
| ი<br>8 | 53.4  | 11.7                | 272                      | 10 | US-09-969-373-608   | Sequence 608, App   |  |
| 9      | 53    | 11.6                | 6030                     | 9  | US-10-239-676-164   | Sequence 164, App   |  |
| 10     | 53    | 11.6                | 15732                    | 9  | US-10-239-676-96    | Sequence 96, Appl   |  |
| 11     | 52.8  | 11.6                | 11047                    | 9  | US-10-239-676-187   | Sequence 187, App   |  |
| 12     | 52.6  | 11.5                | 3991                     | 9  | US-10-074-045-60    | Sequence 60, Appl   |  |
| 13     | 52.4  | 11.5                | 4985                     | 9  | US-10-094-240-10    | Sequence 10, Appl   |  |
| c 14   | 52.2  | 11.4                | 3991                     | 9  | US-10-074-045-60    | Sequence 60, Appl   |  |
| 15     | 52    | 11.4                | 376                      | 10 | us-09-960-352-5087  | Sequence 5087, Ap   |  |
| c 16   | 51.6  | 11.3                | 640681                   | 10 | US-09-790-988-1     | Sequence 1, Appli   |  |
| 17     | 51.4  | 11.3                | 7380                     | 9  | US-10-239-676-66    | Sequence 66, Appl . |  |
| c 18   | 51.4  | 11.3                | 17421                    | 9  | US-10-239-676-54    | Sequence 54, Appl   |  |
| c 19   | 51.2  | 11.2                | 2000                     | 9  | US-09-938-842A-3652 | Sequence 3652, Ap   |  |
|        |       |                     |                          |    |                     |                     |  |

| o o                                    | 0                 |                   |                   |                   | a                 |                   |                   |                   |                   |                   |                    | O                 |                   |                   | a                  | ဂ                 | a                 | a                 |                    |                   | C                   |                   |                   |                   |
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| 44                                     | 43                | 42                | 41                | 40                | 39                | 38                | 37                | 36                | 35                | 34                | ω<br>ω             |                   | 31                | 30                |                    |                   |                   |                   | 25                 | 24                | 23                  | 22                | 21                | 20                |
| 48.4                                   | 48.6              | 48.6              | 48.6              | 48.6              | 48.8              | 48.8              | 48.8              | 48.8              | 49                | 49                | 49                 | 49.4              | 49.4              | 49.4              | 49.4               | 49.6              | 49.6              | 49.6              | 49.6               | 50                | 50                  | 50.2              | 50.4              | 50.6              |
| 10.6<br>10.6                           | 10.7              | 10.7              | 10.7              | 10.7              | 10.7              | 10.7              | 10.7              | 10.7              | 10.7              | 10.7              | 10.7               | 10.8              | 10.8              | 10.8              | 10.8               | 10.9              | 10.9              | 10.9              | 10.9               | 11.0              | 11.0                | 11.0              | 11.1              | 11.1              |
| 12003<br>30350                         | 12405             | 8842              | 7089              | 714               | 7038              | 6815              | 6306              | 5979              | 4187              | 4187              | 960                | 15732             | 15732             | 11036             | 424                | 335913            | 335913            | . 437             | 414                | 5689              | 419                 | 7823              | 640681            | 9515              |
| 9 10                                   | و                 | 9                 | 9                 | 9                 | 9                 | 9                 | 9                 | 9                 | 10                | 9                 | ø                  | 9                 | 9                 | 9                 | 9                  | 9                 | 9                 | 10                | 10                 | 9                 | 10                  | 9                 | 10                | 9                 |
| US-09-764-877-3976<br>US-10-118-328-3  | US-10-239-676-36  | US-10-239-676-71  | US-10-239-676-67  | US-10-060-036-256 | US-10-239-676-204 | US-10-239-676-50  | US-10-239-676-223 | US-10-239-676-18  | US-09-764-855-252 | US-10-072-349-252 | US-10-198-846-6381 | US-10-239-676-96  | US-10-239-676-95  | US-10-239-676-118 | US-10-198-846-2929 | US-09-754-853A-3  | US-09-754-853A-2  | US-09-969-373-937 | US-09-960-352-6528 | US-10-239-676-90  | US-09-960-352-11234 | US-10-239-676-197 | US-09-790-988-1   | US-10-239-676-159 |
| Sequence 3976, Ap<br>Sequence 3, Appli | Sequence 36, Appl | Sequence 71, Appl | Sequence 67, Appl | Sequence 256, App | Sequence 204, App | Sequence 50, Appl |                   | Sequence 18, Appl | Sequence 252, App | Sequence 252, App | Sequence 6381, Ap  | Sequence 96, Appl | Sequence 95, Appl | Sequence 118, App | Sequence 2929, Ap  | Sequence 3, Appli | Sequence 2, Appli | Sequence 937, App | Sequence 6528, Ap  | Sequence 90, Appl | Sequence 11234, A   | Sequence 197, App | Sequence 1, Appli | Sequence 159, App |

# ALIGNMENTS

APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION ONMER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 7035
LENGTH: 858 RESULT 1 US-10-198-846-7035/c Sequence 7035, Application US/10198846 Publication No. US20030099974A1 GENERAL INFORMATION: NAME/KEY: misc\_feature LOCATION: 627, 628, 643, 649, 661, 668, LOCATION: 722, 735, 739, 750, 763, 765, LOCATION: 790, 791, 792, 795, 798, 805, LOCATION: TYPE: DNA ORGANISM: Homo sapiens OTHER INFORMATION: OCATION: LOCATION: NAME/KEY: misc\_feature OCATION: NAME/KEY: misc\_feature OCATION: 393, 398, 459, 466, 517, 526, 576, 588, 57,C or G 184, 185, 236, 237, 279, 281, 338, 349, ,T,C or G 399, 488, 527, 599, 186, 238, 294, 350, 672, 769, 814, 490, 490, 528, 604, 680, 771, 816, 497, 529, 607, 188, 241, 304, 355, 689, 772, 819, 410, 498, 536, 616, 698, 774, 820, 414, 499, 550, 617, 211, 248, 315, 378, 706, 784, 822, 434, 501, 557, 619 212, 250, 318, 379 719, 787, 830, 441, 503, 562,

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; TYPE: DNA; ORGANISM: Artificial Sequence; FEATURE: ; FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-239-676-151
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US-08-781-986A-191
                                              US-08-781-986A-191
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Best Local Similarity
Matches 109; Conserv
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LENGTH: 6327
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 Best Local Similarity
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                                                                                                                                         TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                   NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                FILING DATE:
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11.8%;
46.7%;
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Pred. No. 1
 Score 53.6; DB Pred. No. 3.2;
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В
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                                                                                                                                                       Matches
                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4
LENGTH: 513509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/754,853A CURRENT FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated Witl
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/174,880 PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1119
                                                                                                                                                                                                                                                 LOCATION: (1)..(513509)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
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                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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NAME/KEY: unsure
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                                                                          136361 TTATGTTTAAAATTTTGAATAAATAATTATTTTTGTACGTTCTTTAAAATTGTAGGCCACT
136301 GTCACAATTTAACACATCATAAAATTAAAAAATATAAATAAATTAAATTGTTTAGATTAAAATT
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                                    182 TGAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAAT
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                                                                                                                                                                         Similarity
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APPLICANT: Hauge, Brian M.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping FILE REFERENCE: 38-10(32679)A

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: US 09/754,853

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 09/760,427

PRIOR APPLICATION NUMBER: US 09/855,768

PRIOR APPLICATION NUMBER: US 09/855,768

PRIOR FILING DATE: 2001-05-15
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR PELICATION NUMBER: US 09/760,427
PRIOR PILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 607
LENGTH: 272
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                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
                                                                                                                                                                                                                                                                                                                                        Sequence 608, Application US/09969373 Patent No. US20020133852A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 11.7%;
Best Local Similarity 50.6%;
Matches 129; Conservative
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TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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SEQ ID NOS:
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Pred. No. 1.1;
0; Mismatches 126;
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                                                                                                                                             ; NAME/KEY: unsure
; LOCATION: (5455)
US-10-239-676-164
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US-10-239-676-164
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                                                                           Query Match
' rocal Similarity
                                                                         Matches
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SEQ ID NO 164
LENGTH: 6030
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LENGTH: 272
TYPE: DNA
ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/EP01/03968
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                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                  OTHER INFORMATION:
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DE 10019173.8
DE 10032529.7
DE 10043826.1
                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                       TYPE: DNA
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704 ATTGATTTTTTTAATTGTTGTTTTAGTTTTTGAATTAAGAAAATTGAGTTTTAGAATTAT 763
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                    80 ATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGGAATTAGTATTTTGAGTTTAA 139
                                                                         181;
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o. US20030082609A1
                                                                       Conservative
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                                                                                                                                                                                                          chemically treated genomic DNA (Homo sapiens)
                                                                                    11.68;
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50.6%;
                                                                  Score 53; DB Pred. No. 3.2; O; Mismatches
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                                                                                    DB 9; Length 6030; 3.2;
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NUMBER OF SEQ ID NOS: 2
SEQ ID NO 96
LENGTH: 15732
TYPE: DNA
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Publication No. US20030082609A1
GENERAL INFORMATION:
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Best Local
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, KUIT
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT ENLING ANTE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
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DE 10019173.8
DE 10032529.7
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                                                                                                                                                                                                                   Match 11.6%;
Local Similarity 46.6%;
mes 170; Conservative
                                                                                                                                                          FILING DATE:
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   71 ATACTTGAAATAGCTTAGTTTAAATATAGAATAGCATAATAGATTTTAGGAATTAGTATTT 130
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                                                             TAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAATCGGT
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Pred. No. 4.2; 
0; Mismatches 195; Indels
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Sequence 187, Application US/10239676
Publication No. US20030082609A1
GENERAL INFORMATION:
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SEQ ID NO 187
LENGTH: 11047
TYPE: DNA
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Best Local Similarity
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-99-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/EP01/03968
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                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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DE 10019173.8
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 7942
                                                                                                                   111 GATTTTAGGAATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAAT 170
                51
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GTATATGGTATATAATTAGTGGAGAGAAGTGTATTAGAAAGTTTTAATTTAGAAAT
                                                          TTGAATTTTCGTTAGAGATTT-----TTTTTTATTTTTAAAATTTTTAGAATAGTGTTTG
                                                                                      TCCAAGGCCCATGAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTC 230
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                                                                                                                                                                                                                                         Conservative
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RESULT 12
US-10-074-045-60
; Sequence 60, Application US/10074045
; Publication No. US20030092102A1
; GENERAL INFORMATION:

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Result
No.
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Maximum DB
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Perfect score:
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AL071206 Drosophil
AL077798 Drosophil
AL071865 Drosophil
AL286627 Tetraodon
AL069706 Drosophil
AL106171 Drosophil
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| Drosophil Tetracdon Drosophil Drosophil BOGFE84TF Drosophil BOGFE84TF Drosophil   |  |

## ALIGNMENTS

Drosophila melanogaster.
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101) fly), ge AL071206 GSS. Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr CNS00FYG 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR32N04 of RPCI-98 library from Drosophila melanogaster (fruit Genoscope. AL071206.1 GI:4951245 Direct Submission genomic survey sequence.

SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 CNSOOFYG LOCUS

DEFINITION

COMMENT

REFERENCE AUTHORS

TITLE JOURNAL

Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

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CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10224562 Publication No. US20030022229A1 GENERAL INFORMATION:
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Best Local :
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL00198DIV
                                                                                                                                                                                                                                                                                                   LENGTH: 53332
TYPE: DNA
ORGANISM: Homo sapiens
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nes 144; Conservative
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                                                                                                               AACCTAAAAATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTC 396
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US-10-239-676-151/c
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09801861 Patent No. US20020119544A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Sequence 151, Application US/10239676
Publication No. US20030082609A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.5%;
Best Local Similarity 49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                      PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058 8
DE 10019173.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 53332
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                                                       APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/801,861
CURRENT FILING DATE: 2001-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
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                                                     2000-04-06
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SEQ
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                                                                                                                                 AUTHORS
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                  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 AGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed describtion of the library and how to order individual BAC clones, the entire library; or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS04E5M 976 bp DNA linea:
Tetraodon nigroviridis genome survey sequence T7
103P02 of library G from Tetraodon nigroviridis,
                                       Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                       Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Billault, A., Quetier, F., Sauri
                                                                                                                            2 (bases 1 to 976)
Roest-Crollius, H.,
                                                                                                                                                                                                                                        Roest-Crollius, H., Jaillon, O., Dasilva, C., Bound Bernot, A., Fizames, C., Wincker, P., Brottier, P., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS; genome survey sequence.
Tetraodon nigroviridis.
              Unpublished
                                                                                      Weissenbach, J
                                                                                                                                                                                              Tetraodon nigroviridis
                                                                                                                                                                                                                       Human gene number estimate
                                                                                                                                                                                                                                                                                                          Tetraodontidae; Teti
1 (bases 1 to 976)
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/db_xref="taxon:727"
/db_xref="BACR27A24"
/clone="BACR27A24"
/clone_lib="RRCI-98"
/note="end : T7"
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32.7%;
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Pred. No. 0.0023;
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DNA sequence
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                                                                                                       va,C., Fizames,C., Fi
Saurin,W., Bernot,A.
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r,P., Quetier,
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REFERENCE

JOURNAL TITLE

> Direct Submission Genoscope.

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

SOURCE KEYWORDS VERSION

GSS.

Drosophila melanogaster. AL069706.1 GI:4949849

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

ACCESSION

fly), gen

COMMENT

Determination of this BAC-end Sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's

CNS00EVL/c

CNS00EVL

RESULT 5

DEFINITION

Drosophila melanogaster genome sur BACR29B23 of RPCI-98 library from

1101 bp

p DNA linear GSS 04-JUN-1999 survey sequence T7 end of BAC: rom Drosophila melanogaster (fruit

genomic survey sequence.

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                                                                                                                         744 WAWATTITUTTWAWATTWIWITWATNATAWWIAAWIWTATTITITATTAATAWAW
                                                                                                                                                                                             684
                                                           804 ATTAAATAAATWAATTTTTTTTATAATTTTATTAAWAWWWWIMAWATTTTTATTTA 863
                                                                                 176 GGCCCATGAAAAATTTAATGCTTTATAAGTTTTAAAACTTTACTATATAAAATTTTTCATATG
                                                                                                                                                           123 TAGTATTTTGAGTTTAATTACTTATTGACTTG-----TAACAGTTTTTATAATTCCAA 175
                                                                                                                                                                                                                                                            624
864 TWWTWTNTTTANAAAWTATATAATWATTTTNTTWAAATTTAATTTTAAATTAATAAAT
                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                           3 AAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGC 62
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                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                            MMMMWNWDAAAAMMMTTTTTTWWWTTTTTTWTWTWTTTTNTWWDTWWTTTATTTAT 683
                             TANAATTTAATCGGTATAGTTCGATATTTTTCAATTTATTATTATAAAATAAAAACT 294
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/clone_11b="G"
/note="Genoscope sequence
/nate="137 g 327
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/db_xref="taxon:99883"
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Pred. No. 0.0028;
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    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -

                                                                 Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                        Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 987)
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BACN12P22 of DrosBAC library from Drosophila melanogaster (fr
                                                                                                                                        Genoscope
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                                                                                                                                                                                                                                                                                                                                           fly), genomic survey sequence. AL104456
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/db_xref="taxon:7227"
/clone="BACR27A24"
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/note="end : T7"
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Pred. No. 0.0036;
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Best Local :
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                                                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                              Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                          Direct Submission
Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                          CNSOOLT2 1101 bp DNA linear GSS 14-JUN-1:
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                   fly), genomic survey sequence. AL078714
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/plasmid="pBeloBAC11"
/note="end : SP6"
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/db_xref="taxon:7227"
/clone="BACN12P22"
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31.7%;
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Pred. No. 0.0035;
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Mammoser in Pieter de Jong's laboratory in

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Department

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60
LENGTH: 3991
TYPE: DNA
ORGANISM: Homo sapiens
US-10-074-045-60
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; ORGANISM: Anopheles gambiae
US-10-094-240-10
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                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 10
                                                                                                                                                                          Query Match
                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/094,240
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR FILING DATE: 2002-01-24
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/264,649 PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
FILE REFERENCE: N8289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ21C1
CURRENT APPLICATION NUMBER: US/10/074,045
CURRENT FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                    LENGTH: 4985
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                                                                                                TCATAATCGCTAGAATACTTTGTGCCTTGCTAATAAAGATACTTGAAATAGCTTAGTTTA 92
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                                                                   TTATAGATTTATAAAAATCTACGGTTCTTCAGA 349
                                AATATAAATAGCATAATAGATTTTAGGAATTAGTATTTTGAGTTTAATTACTTATTGACT
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ilarity 49.0%;
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Pred. No. 3.8;
0; Mismatches 146;
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Pred. No. 3.3;
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; TYPE: DNA
; ORGANISM: Homo sapiens
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                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                           Sequence 5087, Application US/09960352 Patent No. US20020137139A1
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Best Local Similarity 52.5%;
Matches 137; Conservative
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NUMBER OF SEQ ID NOS: 74
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                           APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nenghing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CCURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ21C1
NUMBER OF SEQ ID NOS: 15112
EQ ID NO 5087
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Pred. No. 3.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 987)
                                                                                                                                           Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                     Submitted (23-JUL-1999) Genoscope -
BP 191 91006 EVRY cedex - FRANCE (E-
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/clone="BACN11G11"
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                           /clone="BACN12P22"
/clone_lib="DrosBAC"
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                                                                                                                                                                                                              Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a Determination with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/clone="BACN15E10"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
a 103 c 235 g
                                                                                                /organism="Drosophila
/db_xref="taxon:7227"
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Muscomorpha;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopteara; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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Drosophila melanogaster
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL069440.1 GI:4949583
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                                                                /clone_lib="RPCI-98"
/note="end : TET3"
66 c 104 g
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/db_xref="taxon:7227"
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Genoscope

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila.
                                                                                                                                                                                                   and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                      /clone="BACR04A23"
/clone_lib="RPCI-98"
/note="end : TET3"
a 110 c 103 g
                                                                                                                             /organism-"Drosophila
/db_xref="taxon:7227"
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| Search comp  | Db 6                                 | 0у з                            | Db 7:  | 0у 2  | Db 8:  | Qy 11   | Db 8:  | Qy 1:  | Db 9:  | Qy   | Db 99                                       | Qy  | Query Match<br>Best Local :<br>Matches 12  |
|--|--------------------------------------|---------------------------------|--|---|--|---|--|--|--|--|---|---|--|
| Search completed: June 9, 2003, 08:01:26 Job time: 1132 secs | 696 ТАНЖАЛАЛАЛАЛАЛАЛАЛАЛАНЫНЫНЫН 666 | 303 TTATCGGTACAGTTATAGAAAAA 333 | 756 AATAATATAWANAAAAAATTWAWWANATWWWTWWWTAAAAAAAA | 243 TAATCGGTATAGTTCGATATTTTTCAATTTTATTATAAAATAAAAAACTTACCCTAA 302 | 816 TTTAATATATWTAATWTAATWTWWAAAAAAAATAWAAWAWTWAWWWNAWAAAWA 757 | 183 GAAAAATTTAATGCTTTAGTTTTAAACTTTACTATATAAATTTTTTCATATGTAAAATT 242 | 876 AAWAAAAATWAAAAAWNTAWWTATAAWTTWAAAAATWTNTWAWWWAAAAATWWTTT 817 | 123 TAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCAT 182 | 936 AAAAHATAATATATAAAWWTAATWTAATWNATTWAAAAAAATAATAWAATAWWAAATT 877 | 63 TAATAAAGATACTTGAAATAGCTTAAGTTTAAATATAGCATAATAGATTTTAGGAAT 122 | 996 AWAAAAATTWAATAATTAWTATATTNAAAAAAAAAAAAA | 3 AAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGC 62 | Query Match 14.9%; Score 68; DB 17; Length 1101;<br>Best Local Similarity 37.8%; Pred. No. 0.016;<br>Matches 125; Conservative 52; Mismatches 154; Indels 0; Gaps 0; |

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COMMENT
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BP 191 yavo can be received as part of a waw.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruittly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Canada and Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence BACR17N06 of RPCI-98 library from Drosophila
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                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fly), genomic survey sequence. AL077798
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/db_xref="taxon:7227"
/clone="BACR32N04"
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Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP)

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department
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                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                        Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fx
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/db_xref="taxon:7227"
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                                                                                                                                                                Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
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1225 bp DNA linear GSS 26-JUL-19

Drosophila melanogaster genome survey sequence SP6 end of BAC

BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit
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 Determination collaboration
                                               Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                 Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1225)
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Web : www.genoscope.cns.fr)
stermination of this BAC-end sequence was
bilaboration with the European Drosophila
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/clone_lib="RPCI-98"
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDGI The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department
                                                                                                                                                                                                                                 Drosophila melanogaster.
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Inse
Neoptera, Endopterygota, Diptera, Brachycera,
Ephydroidea, Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence T7 end of BAC # BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                              Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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/db_xref="taxon:7227"
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127; Conserv
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                                                                                                                                                                                                                                                                  GSS.
                                                                                                                                                                                                                                                                                                                                         CNS016LI 1101 bp DNA linear GSS 20 Drosophila melanogaster genome survey sequence T7 end of I BACN16D22 of DrosBAC library from Drosophila melanogaster

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was collaboration with the European Drosophila

                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophildae; Drosophila.

1 (bases 1 to 1101)
                                                         Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                   AL106896
AL106896.1
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/db_xref="taxon:7227"
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/clone="BaCR48P19"
/clone_lib="RPCI-98"
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                                                                                                                  Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part
collaboration with the European Drosophila Genome Project (EDGP
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
http://www.edgp.ebi.ac.uk -. This Drosophila delanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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                                                          d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector \mathbf{r}
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Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
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library (Dros BAC) was made by Alain Billaud at CEPH
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/note-"end : T7"
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Pred. No. 0.0068;
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